

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/839,695A
Source: O/PE
Date Processed by STIC: 6/3/2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/839,695A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino
Numbering The numbering under each 3rd amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

RAW SEQUENCE LISTING

DATE: 06/03/2003

PATENT APPLICATION: US/09/839,695A

TIME: 13:13:42

Input Set : A:\PTO.PG.txt

Output Set: N:\CRF4\06032003\I839695A.raw

2 <110> APPLICANT: Balaban, Naomi
 3 Larrick, James W. Wright, Susan C.
 W--> 4 <120> TITLE OF INVENTION: Methods and Compositions for the
 W--> 5 Treatment and Prevention of Staphylococcus Aureus Infections
 W--> 6 <130> FILE REFERENCE: BALA-001CIP
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/839,695A
 C--> 7 <141> CURRENT FILING DATE: 2001-04-19
 7 <150> PRIOR APPLICATION NUMBER: 60/068,094
 8 <151> PRIOR FILING DATE: 1997-12-19
 9 <150> PRIOR APPLICATION NUMBER: 09/054,331
 10 <151> PRIOR FILING DATE: 1998-04-02
 W--> 11 <160> NUMBER OF SEQ ID: 15
 12 <170> SOFTWARE: FastSEQ for Windows Version 4.0

*see item 4
on Error Summary
Sheet*

ERRORED SEQUENCES

W--> 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 7
 15 <212> TYPE: PRT
 16 <213> ORGANISM: S. aureus
 W--> 17 <220> FEATURE:
 18 <221> NAME/KEY: VARIANT
 19 <222> LOCATION: (1)...(7)
 20 <223> OTHER INFORMATION: Xaa = Cys, Trp or Ile

pgs 1-5
Does Not Comply
Corrected Diskette Needed

*Per 1.824
of Sequence Rules,
please attach
a label to
submitted
computer
readable
form*

W--> 21 <400> SEQUENCE: 1
 W--> 22 Tyr Lys Pro Xaa Thr Asn Phe
 E--> 23 1 5
 24 <210> SEQ ID NO: 2
 25 <211> LENGTH: 7
 26 <212> TYPE: PRT
 27 <213> ORGANISM: S. aureus
 W--> 28 <220> FEATURE:
 29 <221> NAME/KEY: VARIANT
 30 <222> LOCATION: (1) ... (7)
 31 <223> OTHER INFORMATION: Xaa = Cys, Trp or Ile

W--> 32 <400> SEQUENCE: 2
 W--> 33 Tyr Ser Pro Xaa Thr Asn Phe
 E--> 34 1 5
 35 <210> SEQ ID NO: 3
 36 <211> LENGTH: 10
 37 <212> TYPE: PRT
 38 <213> ORGANISM: S. aureus

*see item 3 on Error Summary
Sheet*

*see item 3 (global error)
see following pages*

RAW SEQUENCE LISTING

DATE: 06/03/2003

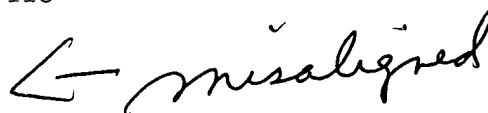
PATENT APPLICATION: US/09/839,695A

TIME: 13:13:42

Input Set : A:\PTO.PG.txt

Output Set: N:\CRF4\06032003\I839695A.raw

40 <220> FEATURE:
43 <221> NAME/KEY: VARIANT
44 <222> LOCATION: (1) ...(10)
45 <223> OTHER INFORMATION: Xaa = Cys, Trp or Ile
W--> 46 <400> SEQUENCE: 3
W--> 47 Ile Lys Lys Tyr Lys Pro Xaa Thr Asn Phe
E--> 48 1 5 10
49 <210> SEQ ID NO: 4
50 <211> LENGTH: 10
51 <212> TYPE: PRT
52 <213> ORGANISM: S. aureus
W--> 53 <220> FEATURE:
54 <221> NAME/KEY: VARIANT
55 <222> LOCATION: (1) ... (10)
56 <223> OTHER INFORMATION: Xaa = Cys, Trp or Ile
W--> 57 <400> SEQUENCE: 4
W--> 58 Ile Lys Lys Tyr Ser Pro Xaa Thr Asn Phe
E--> 59 1 5 10
66 <210> SEQ ID NO: 6
67 <211> LENGTH: 9
68 <212> TYPE: PRT
69 <213> ORGANISM: S. aureus
W--> 70 <400> SEQUENCE: 6
71 Ile Lys Lys Tyr Lys Pro Ile Thr Asn
E--> 72 1 5
73 <210> SEQ ID NO: 7
74 <211> LENGTH: 7
75 <212> TYPE: PRT
76 <213> ORGANISM: Artificial Sequence
W--> 77 <220> FEATURE:
78 <223> OTHER INFORMATION: synthetic peptide
W--> 79 <400> SEQUENCE: 7
80 Tyr Ser Pro Trp Thr Asn Phe
E--> 81 1 5
82 <210> SEQ ID NO: 8
83 <211> LENGTH: 5
84 <212> TYPE: PRT
85 <213> ORGANISM: Artificial Sequence
W--> 86 <220> FEATURE:
89 <223> OTHER INFORMATION: synthetic peptide
W--> 90 <400> SEQUENCE: 8
91 Pro Cys Thr Asn Phe
E--> 92 1 5
93 <210> SEQ ID NO: 9
94 <211> LENGTH: 7
95 <212> TYPE: PRT
96 <213> ORGANISM: S. aureus
W--> 97 <400> SEQUENCE: 9
98 Tyr Lys Pro Ile Thr Asn Phe

A handwritten signature in cursive script that reads "misaligned". A large arrow points from the signature towards the sequence alignment area, specifically pointing to the "5" in the sequence "1 5 10" on line 48.

RAW SEQUENCE LISTING

DATE: 06/03/2003

PATENT APPLICATION: US/09/839,695A

TIME: 13:13:42

Input Set : A:\PTO.PG.txt

Output Set: N:\CRF4\06032003\I839695A.raw

```

E--> 99 1 5
      100 <210> SEQ ID NO: 10
      101 <211> LENGTH: 7
      102 <212> TYPE: PRT
      103 <213> ORGANISM: Artificial Sequence
W--> 104 <220> FEATURE:
      105 <223> OTHER INFORMATION: synthetic peptide
W--> 106 <400> SEQUENCE: 10
      107 Tyr Ser Pro Ile Thr Asn Phe
E--> 108 1 5
      109 <210> SEQ ID NO: 11
      110 <211> LENGTH: 7
      111 <212> TYPE: PRT
      112 <213> ORGANISM: Artificial Sequence
W--> 113 <220> FEATURE:
      114 <223> OTHER INFORMATION: synthetic peptide
W--> 115 <400> SEQUENCE: 11
      116 Tyr Lys Pro Trp Thr Asn Phe
E--> 117 1 5
      141 <210> SEQ ID NO: 13
      142 <211> LENGTH: 279
      143 <212> TYPE: PRT
      144 <213> ORGANISM: Staphylococcus spp
W--> 145 <400> SEQUENCE: 13
      146 Met Ala Ile Lys Lys Tyr Lys Pro Ile Thr Asn Gly Arg Arg Asn Met
E--> 147 1 5 10 15
      148 Thr Ser Leu Asp Phe Ala Glu Ile Thr Lys Thr Thr Pro Glu Lys Ser
E--> 149 20 25 30
      150 Leu Leu Lys Pro Leu Pro Lys Lys Ala Gly Arg Asn Asn Gln Gly Lys
E--> 151 35 40 45
      152 Leu Thr Val Arg His His Gly Gly Gly His Lys Arg Gln Tyr Arg Val
E--> 153 50 55 60
      154 Ile Asp Phe Lys Arg Asn Lys Asp Gly Ile Asn Ala Lys Val Asp Ser
E--> 155 65 70 75 80
      156 Ile Gln Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Val Tyr
E--> 157 85 90 95
      158 Ala Asp Gly Glu Lys Arg Ile Tyr His Cys Ile Ala Pro Lys Gly Leu
E--> 159 100 105 110
      160 Glu Val Gly Gln Ile Val Glu Ser Gly Ala Glu Ala Asp Thr Lys Val
E--> 161 115 120 125
      162 Gly Asn Ala Leu Pro Leu Gln Asn Ile Pro Val Gly Thr Val Val His
E--> 163 130 135 140
      164 Asn Ile Glu Leu Lys Pro Gly Lys Gly Gly Gln Ile Ala Arg Ser Ala
E--> 165 145 150 155 160
      166 Gly Ala Ser Ala Gln Val Leu Gly Lys Glu Gly Lys Tyr Val Leu Ile
E--> 167 165 170 175
      168 Arg Leu Arg Ser Gly Glu Val Arg Met Ile Leu Ser Thr Cys Arg Ala
E--> 169 180 185 190
      170 Thr Ile Gly Gln Val Gly Asn Leu Gln His Glu Leu Val Asn Val Gly

```

RAW SEQUENCE LISTING

DATE: 06/03/2003

PATENT APPLICATION: US/09/839,695A

TIME: 13:13:42

Input Set : A:\PTO.PG.txt

Output Set: N:\CRF4\06032003\I839695A.raw

E--> 171 195 200 205
172 Lys Ala Gly Arg Ser Arg Trp Lys Gly Ile Arg Pro Thr Val Arg Gly
E--> 173 210 215 220
174 Ser Val Met Asn Pro Asn Asp His Pro His Gly Gly Gly Glu Gly Arg
E--> 175 225 230 235 240
176 Ala Pro Ile Gly Arg Pro Ser Pro Met Ser Pro Trp Gly Lys Pro Thr
E--> 177 245 250 255
178 Leu Gly Lys Lys Thr Arg Arg Gly Lys Lys Ser Ser Asp Lys Leu Ile
E--> 179 260 265 270
180 Val Arg Gly Arg Lys Lys Lys
E--> 181 275
191 <210> SEQ ID NO: 15
192 <211> LENGTH: 32
193 <212> TYPE: DNA
194 <213> ORGANISM: Artificial Sequence
W--> 195 <220> FEATURE:
196 <223> OTHER INFORMATION: Primer
W--> 197 <400> SEQUENCE: 15
198 cgcgcggatc cttatttttt cttacgtcca cg 32
E--> 201 1

*delete**see p. 5 for more error*

09/839695A 5

<210> 14

<211> 30

<212> DNA

<213> ~~Prim~~Artificial Sequence

delete

VERIFICATION SUMMARY

DATE: 06/03/2003

PATENT APPLICATION: US/09/839,695A

TIME: 13:13:43

Input Set : A:\PTO.PG.txt

Output Set: N:\CRF4\06032003\I839695A.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application No
L:7 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:13 M:283 W: Missing Blank Line separator, <210> field identifier
L:17 M:283 W: Missing Blank Line separator, <220> field identifier
L:21 M:283 W: Missing Blank Line separator, <400> field identifier
L:22 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:23 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
M:332 Repeated in SeqNo=2
L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
M:332 Repeated in SeqNo=3
L:53 M:283 W: Missing Blank Line separator, <220> field identifier
L:57 M:283 W: Missing Blank Line separator, <400> field identifier
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
M:332 Repeated in SeqNo=4
L:64 M:283 W: Missing Blank Line separator, <400> field identifier
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:72 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:77 M:283 W: Missing Blank Line separator, <220> field identifier
L:79 M:283 W: Missing Blank Line separator, <400> field identifier
L:81 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:86 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:283 W: Missing Blank Line separator, <400> field identifier
L:92 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:97 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:104 M:283 W: Missing Blank Line separator, <220> field identifier
L:106 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:113 M:283 W: Missing Blank Line separator, <220> field identifier
L:115 M:283 W: Missing Blank Line separator, <400> field identifier
L:117 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:122 M:283 W: Missing Blank Line separator, <400> field identifier
L:145 M:283 W: Missing Blank Line separator, <400> field identifier
L:147 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
M:332 Repeated in SeqNo=13
L:185 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:14
L:186 M:283 W: Missing Blank Line separator, <220> field identifier
L:195 M:283 W: Missing Blank Line separator, <220> field identifier
L:197 M:283 W: Missing Blank Line separator, <400> field identifier
L:201 M:254 E: No. of Bases conflict, this line has no nucleotides.